Identification of three QTLs with influence on susceptibility to helminth infections in pigs

Nejsum, Peter; Thamsborg, Stig Milan; Göring, H. H.; Karlskov-Mortensen, Peter; Archibald, A. L.; Roepstorff, Allan Knud; Anderson, T. J. C.; Fredholm, Merete; Jørgensen, Claus Bøttcher

Publication date:
2010

Document version
Publisher's PDF, also known as Version of record

of control efforts, has stabilized into a permanent transmission cycle in the Zoo's chimpanzee troop.

16. P. IDENTIFICATION OF THREE QTLS WITH INFLUENCE ON SUSCEPTIBILITY TO HELMINTH INFECTIONS IN PIGS

[1]Nejsum, P.; [1]Thamsborg, S. M.; [2]Göring, H. H.; [3]Karlskov-Mortensen, P.; [4]Archibald, A. L.; [1]Roepstorff, A.; [2]Anderson,T. J. C.; Fredholm[3], M. and [3]Jørgensen, C. B.
[1)] Parasitology, Health and Development, Department of Veterinary Disease Biology, Faculty of Life Sciences, University of Copenhagen, Dyrlægevej 100, DK-1870 Frederiksberg C, Denmark. [2)] Southwest Foundation for Biomedical Research, Genetics, 7620 NW Loop 410, San Antonio, TX 78245-0549, USA. [3)] Basic Animal and Veterinary Sciences/Genetics & Bioinformatics, Faculty of Life Sciences, University of Copenhagen, Grønnegårdsvej 3, 1870 Frederiksberg C, Denmark. [4)] The Roslin Institute, University of Edinburgh, Genetics and Genomics, Roslin, Midlothian EH25 9PS, United Kingdom

Abstract
Intestinal helminth infections are causing health and welfare problems in both human and animal populations. A family, in which susceptibility towards *Ascaris* (large round worm) and *Trichuris* (whipworm) infections are segregating, was constructed. Our data demonstrate that genetic components are responsible for approximately 45% and 70% of the variation in *Ascaris* and *Trichuris* parasite loads, respectively. A genome scan using the Ilummina 7K SNP-chip has been performed in order to locate genomic regions controlling this susceptibility. A total of 194 pigs from 19 full-sib litters have been genotyped and 3955 informative SNPs were used to perform genotype association analysis. For *Trichuris* parasite load (faecal egg excretion) four SNPs in a 2 Mb region on SSC13 and 4 SNPs in a 7 Mb region on SSC11 have been identified, whereas 7 SNPs located within a 6 Mb region on SSC4 were associated with *Ascaris* egg excretion and worm load. The proportion of phenotypic variance accounted for by a SNP's genotype ranged from 0.08-0.14 and 0.06-0.12 for *Ascaris* and *Trichuris,* respectively. The identified QTLs will be verified in unrelated pig material and we are currently collecting samples for that purpose. Re-sequencing technology will be applied in candidate regions on pigs with deviating phenotypes, which will provide information on all genetic differences in the genomic regions.

17. O. EFFICACY OF SINGLE AND DOUBLE DOSES OF ALBENDAZOLE AND MEBENDAZOLE ALONE AND IN COMBINATION IN THE TREATMENT OF *TRICHURIS TRICHIURA* INFECTION IN SCHOOL AGED CHILDREN IN UGANDA.

*Harriet Namwanje [a], Narcis Kabatereine [a], Annette Olsen [b]
[a] Vector Control Division, Ministry of Health, Kampala, Uganda. [b] DBL-Centre for Health Research and Development, Department of Disease Biology, Faculty of Life Sciences, University of Copenhagen, Denmark.